

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Weininger, Susan
Weininger, Arthur M

(ii) TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION

(iii) NUMBER OF SEQUENCES: 118

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Saliwanchik & Saliwanchik
(B) STREET: 2421 N.W. 41st St., Suite A-1
(C) CITY: Gainesville
(D) STATE: Florida
(E) COUNTRY: USA
(F) ZIP: 32606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/860,844
(B) FILING DATE: 09-JUN-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/353,476
(B) FILING DATE: 09-DEC-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Saliwanchik, David R.
(B) REGISTRATION NUMBER: 35,746
(C) REFERENCE/DOCKET NUMBER: GP-100C1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (352) 375-8100
(B) TELEFAX: (352) 372-5800

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGGGATTCC CCA

13

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGGGACTTT CCC

13

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGGGGACTTT CCG

13

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTGGGGACT TTCCA

15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

A / ACAAGGGACT TTCCG

15

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGGTTTTC CCC

13

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

A1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGGGACTTT CCGCTGGGGA CTTTCCA

27

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGGGACTTT CCGCTGGGGA CTTTCCG

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGGGGACT TTCCAGGGAG GCGTGG

26

(2) INFORMATION FOR SEQ ID NO:10:

- G /
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTGGGGACT TTCCAGGGGA GGTGTG

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTGGGGACT TTCCGGGGAG CGTGGC

26

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTGGGGACT TTCCGGGGAG GCGCGG

26

A1.
(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCTGGGGACT TTCCAGAGAG GCGTGG

26

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTGGGGACT TTCCAGGGGA GGCGTG

26

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCTGGGGACT TTCCAGGGAG GCGTGG

26

C1
(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCTGGGGACT TTCCAGGGAG GCTGCC

26

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTTCCAGGGA GGC GTGGCCT GGG CGGGACT GGG

33

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGTGGCCTGG CGGGACTGG GGAGTGGCGT CCC

33

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCT

45

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGCAAGGGA CTTTCCGCTG GGGACTTCC AGGGGAGGTG TGGCCT

46

(2) INFORMATION FOR SEQ ID NO:21:

- G /
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CATCAAGGGA CTTTCCGCTG GGGACTTCC AGGGGAGGTG TGGCCT

46

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGTG TGGCCT

46

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

C₁ / CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCAT

45

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC GGGGAGCGTG GCCT

44

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC GGGGAGGCAGC GGCT

44

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGAGAGGCAGT GGACT

45

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGCAGT TGGACT

46

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTACAGGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCCT GGGGAG

46

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTACAGGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCTG CCT

43

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTTTCCGCTG GGGACTTCC AGGGAGGCCGT GGCTGGCG GGACTGGG

48

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTCCAGGGA GGC GTGGC CT GGG CGG GACT GGG GAGTGGC GTCCC

45

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTACAAGGGA CTTTCCGCTG GGGACTTCC AGGGAGGCCGT GGCTGGCG GGACTGGG

59

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTTCCGCTGG GGACTTTCCA GGGAGGCGTG GCCTGGCGG GACTGGGGAG TGGCGTCCC 59

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCTGGCGG GGACTGGGA 60

GTTGGCGTCCC 70

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TATCACCGCC AGTGGTATTG ATGTCAACAC CGCCAGAGAT AATTATCAC CGCAGATGGT 60

T

61

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TATCACCGCA AGGGATAAAAT ATCTAACACC GTGCGTGTG ACTATTTAC CTCTGGCGGT 60

GATA 64

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CTACAAGGGA CTTTCCGCTG GGGACTTCAGGGAGGCGT GGCTGGCG GGACTGGGGA 60

GTGGCGTCCC 70

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGG

37

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGGGACTGGG GAGTGGCGTC CC

22

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGTAT CACCGCCAGT GGTATTTATG

60

TCAACACCGC CAGAGATAAT TTATCACCGC AGATGGTTCT GCA

103

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAACCATCTG CGGTGATAAA TTATCTCTGG CGGTGTTGAC ATAAATACCA CTGGCGGTGA	60
TA	62

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCCAACCA TCTGCGGTGA TAAATTATCT CTGGCGGTGT TGACATAAAT ACCACTGGCG	60
TGATGACTGC A	71

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTATCACCGC CAGTGGTATT TATGTCAACA CCGCCAGAGA TAATTTATCA CCGCAGATGG 60

TTG 63

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GATCCGGGGG GATACCCCC G 21

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGGACTGGG GAGTGGCGTC CCTATCACCG CAAGGGATAA ATATCTAACCA CCGTGCGTGT 60

TGACTATTTT ACCTCTGGCG GTGATAGCAT G

91

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTAAGGGCGT AACCGAAATC GGTTGAACCG AAACCGGTTA GTATAAAAGC AGA

53

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAAAGGGAGT AACCGAAAAC GGTCGGGACC GAAAACGGTG TATATAAAAG ATGT

54

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AGTAGGGTGT AACCGAAAGC GGTTCAACCG AAAACGGTGC ATATATAAAG CAAA

54

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCTTCAACCG AATTCCGGTTG CATG

24

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGTGCAACCG ATTTCCGGTTG CCTT

24

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TATGCAACCG AAATAGGTTG GGCA

24

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGCCTAACCG TTTTCGGTTA CTTG

24

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGACTAACCG TTTTAGGTCA TATT

24

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GACGACTATC CAGCGACCAA GATCAGAGCC AGACACCGGA AACCCCTGCC AC

52

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GACGACACGG TATCCGCTAC TCAGCTTGTAAACAGCTAC AGCACACCCCC CTC

53

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GACGACGACC TGCAGACACC ACAGACACCG CCCAGCCCT TACAAAGCTG TTCTGTGCAG 60

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CATACCAAAG CCGTCGCCTT GGGCACCGAA GAAACACAAC CACTAAGTTG TTGCACAGAG 60

ACTCAGTG 68

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TAATGTAATT GATTGTAATG ACTCTATGTG CAGTACCAAGT ACCGTATTCC AGCACCGTGT 60

CCGTGGGCAC CGCAAAG 77

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAGACAACG ATAACCGACC ACCACAAGCA GCGGCCAAC ACCCCGCCTT GGACAATAGA	60
ACAGCACGT A CTGCAACTAA	80

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CATATGCAAT ACAATGCATT ATACAAACTG GACACATATA TATATTGTG AAGAAGCATC	60
AGTAACGTG GTAGAGGGTC AAGTTGACTA TTATGGTTA TATTATGTTC ATGAAGGAAT	120
ACGAACATAT TTTGTGCAGT TTAAAGATGA TGCAAAAAA TATAGTAAAA ATAAAGTATG	180
GGAAGTTCAT GCGGGTGGTC AGGTAATATT ATGTCCTACA TCTGTGTTA GCAGCAACGA	240
AGTATCCTCT CCTGAAATTA TTAGGC	266

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 95 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AGGATGTATA AAAAAACATG GATATACAGT GGAAGTGCAG TTTGATGGAG ACATATGCTA 60

TTAGGCAGCA CTTGGCCAAC CACCCCGCCG CGACC 95

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CATGTTTTTT TATACATCCA TATCACCGCC AGTGGTATTG ATGTCAACAC CGCCAGAGAT 60

AATTTATCAC CGCAGATGGT T 81

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Ala Asp Asp Asp Pro Tyr Gly Thr Gly Gln Met Phe His Leu Asn
1 5 10 15

Thr Ala Leu Thr His Ser Ile Phe Asn Ala Glu Leu Tyr Ser Pro Glu
20 25 30

Ile Pro Leu Ser Thr Asp Gly Pro Tyr Leu Gln Ile Leu Glu Gln Pro
35 40 45

Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly Pro Ser His
50 55 60

Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys Ser Tyr Pro
65 70 75 80

Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val Ile Val Gln
85 90 95

Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His Ser Leu Val
100 105 110

Gly Lys His Cys Glu Asp Gly Val Cys Thr Val Thr Ala Gly Pro Lys
115 120 125

Asp Met Val Val Gly Phe Ala Asn Leu Gly Ile Leu His Val Thr Lys
130 135 140

Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu Ala Cys Ile
145 150 155 160

Arg Gly Tyr Asn Pro Gly Leu Leu Val His Ser Asp Leu Ala Tyr Leu
165 170 175

Gln Ala Glu Gly Gly Asp Arg Gln Leu Thr Asp Arg Glu Lys Glu
180 185 190

Ile Ile Arg Gln Ala Ala Val Gln Gln Thr Lys Glu Met Asp Leu Ser
195 200 205

Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser Thr Gly Ser
210 215 220

Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile Tyr Asp Ser
225 230 235 240

Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met Asp Arg Thr
245 250 255

Ala Gly Cys Val Thr Gly Gly Glu Ile Tyr Leu Leu Cys Asp Lys
260 265 270

Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu Glu Asn
275 280 285

Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr Asp Val His
290 295 300

Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys Asp Val Asn
305 310 315 320

Ile Thr

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Ala Glu Asp Asp Pro Tyr Leu Gly Arg Pro Glu Gln Met Phe His
1 5 10 15

Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val Phe Gln
20 25 30

Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln Ile Leu
35 40 45

Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Tyr Val Cys Glu Gly
50 55 60

Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys
65 70 75 80

Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val
85 90 95

Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His
 100 105 110

Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val Thr Ala
 115 120 125

Gly Pro Glu Asp Cys Val His Gly Phe Ala Asn Leu Gly Ile Leu His
 130 135 140

Val Thr Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu
 145 150 155 160

Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro Asp Leu
 165 170 175

Ala Tyr Leu Gln Ala Glu Gly Gly Asp Arg Gln Leu Gly Asp Arg
 180 185 190

Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys Glu Met
 195 200 205

Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser
 210 215 220

Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile
 225 230 235 240

Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met
 245 250 255

Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu
 260 265 270

Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu
 275 280 285

Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr
 290 295 300

Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys
 305 310 315 320

Asp Ile Asn Ile Thr
 325

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Glu Pro Ala Asp Leu Leu Pro Leu Tyr Leu Gln Pro Glu Trp Gly
1 5 10 15

Glu Gln Glu Pro Gly Gly Ala Thr Pro Phe Val Glu Ile Leu Glu Gln
20 25 30

Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser
35 40 45

Ala Gly Ser Ile Pro Gly Glu His Ser Thr Asp Ser Ala Arg Thr His
50 55 60

Pro Thr Ile Arg Val Asn His Tyr Arg Gly Pro Gly Arg Val Arg Val
65 70 75 80

Ser Leu Val Thr Lys Asp Pro Pro His Gly Pro His Pro His Glu Leu
85 90 95

Val Gly Arg His Cys Gln His Gly Tyr Tyr Glu Ala Glu Leu Ser Pro
100 105 110

Asp Arg Ser Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys
115 120 125

Lys Arg Glu Leu Glu Ala Ala Val Ala Glu Arg Ile Arg Thr Asn Asn
130 135 140

Asn Pro Phe Asn Val Pro Met Glu Glu Arg Gly Ala Glu Tyr Asp Leu
145 150 155 160

Ser Ala Val Arg Leu Cys Phe Gln Val Trp Val Asn Gly Pro Gly Gly
165 170 175

Leu Cys Pro Leu Pro Pro Val Leu Ser Gln Pro Ile Tyr Asp Asn Arg
180 185 190

Ala Pro Ser Thr Ala Glu Leu Arg Ile Leu Pro Gly Asp Arg Asn Ser
195 200 205

Gly Ser Cys Gln Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val
210 215 220

Gln Lys Glu Asp Ile Glu Val Arg Phe Trp Ala Glu Gly Trp Glu Ala
225 230 235 240

Lys Gly Ser Phe Ala Ala Ala Asp Val His Arg Gln Val Ala Ile Val
245 250 255

Phe Arg Thr Pro Pro Phe Arg Glu Arg Ser Leu Arg
260 265

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Asp Asp Leu Phe Pro Leu Ile Phe Pro Ser Glu Pro Ala Gln Ala
1 5 10 15

Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met
20 25 30

Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
35 40 45

Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
50 55 60

Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
65 70 75 80

Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
85 90 95

Asp Gly Tyr Tyr Glu Ala Asp Leu Cys Pro Asp Arg Ser Ile His Ser
100 105 110

Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
115 120 125

Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe His Val Pro
130 135 140

Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
145 150 155 160

Phe Gln Val Thr Val Arg Asp Pro Ala Gly Arg Pro Leu Leu Thr
165 170 175

Pro Val Leu Ser His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
180 185 190

Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly
195 200 205

Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile
210 215 220

Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser
225 230 235 240

Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
245 250 255

Tyr Ala Asp Pro Ser Leu Gln
260

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 263 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Asp Glu Leu Phe Pro Leu Ile Phe Pro Ala Glu Pro Ala Gln Ala
1 5 10 15

Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met
 20 25 30

Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
 35 40 45

Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
 50 55 60

Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
 65 70 75 80

Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
 85 90 95

Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser
 100 105 110

Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
 115 120 125

Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro
 130 135 140

Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
 145 150 155 160

Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro
 165 170 175

Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
 180 185 190

Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly
 195 200 205

Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile
 210 215 220

Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser
 225 230 235 240

Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
 245 250 255

Tyr Ala Asp Pro Ser Leu Gln
 260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Phe	Pro	Asn	Gln	Asn	Asn	Gly	Ala	Ala	Pro	Gly	Gln	Gly	Pro	Ala
1				5					10					15	
Val	Asp	Gly	Gln	Gln	Ser	Leu	Asn	Tyr	Asn	Gly	Leu	Pro	Ala	Gln	Gln
					20			25						30	
Gln	Gln	Gln	Leu	Ala	Gln	Ser	Thr	Lys	Asn	Val	Arg	Lys	Lys	Pro	Tyr
			35				40					45			
Val	Lys	Ile	Thr	Glu	Gln	Pro	Ala	Gly	Lys	Ala	Leu	Arg	Phe	Arg	Tyr
	50				55						60				
Glu	Cys	Glu	Gly	Arg	Ser	Ala	Gly	Ser	Ile	Pro	Gly	Val	Asn	Ser	Thr
	65				70				75				80		
Pro	Glu	Asn	Lys	Thr	Tyr	Pro	Thr	Ile	Glu	Ile	Val	Gly	Tyr	Lys	Gly
			85				90					95			
Arg	Ala	Val	Val	Val	Val	Ser	Cys	Val	Thr	Lys	Asp	Thr	Pro	Tyr	Arg
		100						105				110			
Pro	His	Pro	His	Asn	Leu	Val	Gly	Lys	Glu	Gly	Cys	Lys	Lys	Gly	Val
				115				120				125			
Cys	Thr	Leu	Glu	Ile	Asn	Ser	Glu	Thr	Met	Arg	Ala	Val	Phe	Ser	Asn
		130				135				140					
Leu	Gly	Ile	Gln	Cys	Val	Lys	Lys	Lys	Asp	Ile	Glu	Ala	Ala	Leu	Lys
	145				150				155				160		
Ala	Arg	Glu	Glu	Ile	Arg	Val	Asp	Pro	Phe	Lys	Thr	Gly	Phe	Ser	His
			165					170				175			
Arg	Phe	Gln	Pro	Ser	Ser	Ile	Asp	Leu	Asn	Ser	Val	Arg	Leu	Cys	Phe
			180					185				190			

Gln Val Phe Met Glu Ser Glu Gln Lys Gly Arg Phe Thr Ser Pro Leu
195 200 205

Pro Pro Val Val Ser Glu Pro Ile Phe Asp Lys Lys Ala Met Ser Asp
210 215 220

Leu Val Ile Cys Arg Leu Cys Ser Cys Ser Ala Thr Val Phe Gly Asn
225 230 235 240

Thr Gln Ile Ile Leu Leu Cys Glu Lys Val Ala Lys Glu Asp Ile Ser
245 250 255

Val Arg Phe Phe Glu Glu Lys Asn Gly Gln Ser Val Trp Glu Ala Phe
260 265 270

Gly Asp Phe Gln His Thr Asp Val His Lys Gln Thr Ala Ile Thr Phe
275 280 285

Lys Thr Pro Arg Tyr His Thr Leu Asp Ile Thr
290 295

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Asp Phe Leu Thr Asn Leu Arg Phe Thr Glu Gly Ile Ser Glu Pro
1 5 10 15

Tyr Ile Glu Ile Phe Glu Gln Pro Arg Gln Arg Gly Thr Arg Phe Arg
20 25 30

Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly Glu His Ser
35 40 45

Thr Asp Asn Asn Lys Thr Phe Pro Ser Ile Gln Ile Leu Asn Tyr Phe
50 55 60

Gly Lys Val Lys Ile Arg Thr Thr Leu Val Thr Lys Asn Glu Pro Tyr
65 70 75 80

Lys Pro His Pro His Asp Leu Val Gly Lys Gly Cys Arg Asp Gly Tyr
85 90 95

Tyr Glu Ala Glu Phe Gly Pro Glu Arg Gln Val Leu Ser Phe Gln Asn
100 105 110

Leu Gly Ile Gln Cys Val Lys Lys Asp Leu Lys Glu Ser Ile Ser
115 120 125

Leu Arg Ile Ser Lys Lys Asn Pro Phe Asn Val Pro Glu Glu Gln Leu
130 135 140

His Asn Ile Asp Glu Tyr Asp Leu Asn Val Val Arg Leu Cys Phe Gln
145 150 155 160

Ala Phe Leu Pro Asp Glu His Gly Asn Tyr Thr Leu Ala Leu Pro Pro
165 170 175

Leu Ile Ser Asn Pro Ile Tyr Asp Asn Arg Ala Pro Asn Thr Ala Glu
180 185 190

Leu Arg Ile Cys Arg Val Asn Lys Asn Cys Gly Ser Val Lys Gly Gly
195 200 205

Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Asp Asp Ile Glu
210 215 220

Val Arg Phe Val Leu Gly Asn Trp Glu Ala Lys Gly Ser Phe Ser Gln
225 230 235 240

Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro Phe
245 250 255

Leu Gly Asp Ile Thr
260

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Asp Phe Leu Thr Asn Leu Arg Phe Thr Glu Gly Ile Ser Glu Pro
1 5 10 15

Tyr Ile Glu Ile Phe Glu Gln Pro Arg Gln Arg Gly Met Arg Phe Arg
20 25 30

Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly Glu His Ser
35 40 45

Thr Asp Asn Asn Lys Thr Phe Pro Ser Ile Gln Ile Leu Asn Tyr Phe
50 55 60

Gly Lys Val Lys Ile Arg Thr Thr Leu Val Thr Lys Asn Glu Pro Tyr
65 70 75 80

Lys Pro His Pro His Asp Leu Val Gly Lys Gly Cys Arg Asp Gly Tyr
85 90 95

Tyr Glu Ala Glu Phe Gly Pro Glu Arg Gln Val Leu Ser Phe Gln Asn
100 105 110

Leu Gly Ile Gln Cys Val Lys Lys Lys Asp Leu Lys Glu Ser Ile Ser
115 120 125

Leu Arg Ile Ser Lys Lys Ile Asn Pro Phe Asn Val Pro Glu Glu Gln
130 135 140

Leu His Asn Ile Asp Glu Tyr Asp Leu Asn Val Val Arg Leu Cys Phe
145 150 155 160

Gln Ala Phe Leu Pro Asp Glu His Gly Asn Tyr Thr Leu Ala Leu Pro
165 170 175

Pro Leu Ile Ser Asn Pro Ile Tyr Asp Asn Arg Ala Pro Asn Thr Ala
180 185 190

Glu Leu Arg Ile Cys Arg Val Asn Lys Asn Cys Gly Ser Val Lys Gly
195 200 205

Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Asp Asp Ile
210 215 220

Glu Val Arg Phe Val Leu Gly Asn Trp Glu Ala Lys Gly Ser Phe Ser
225 230 235 240

Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
245 250 255

Phe Leu Gly Asp Ile Thr
260

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu Ser
145 150 155 160

His Phe Pro Tyr Val Leu Phe Leu Glu Gly Ser Asn Phe Leu Thr Glu
165 170 175

Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu Tyr
180 185 190

Asn Ser Gly Ser Glu Ser His Phe Pro Tyr Val Leu Phe Leu Glu Gly
195 200 205

Ser Asn Phe Leu Thr Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg
210 215 220

Val Val Asn Leu Glu Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg
225 230 235 240

Leu Thr Ala Ala Asn Tyr Gly Met Pro Ile Asn Ser Asn Leu Cys Ile
245 250 255

Asn Lys Phe Val Asn His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala
260 265 270

Ser Ile Tyr Thr Gln Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met
275 280 285

Phe Glu Ile Met Phe Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly
290 295 300

Arg Asp Leu Phe Glu Gln Leu Thr Ser Lys
305 310

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Cys Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg Lys
1 5 10 15

Thr

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Asp Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly Cys
1 5 10 15

Gly Lys Val Tyr Gly Lys Thr Ser His Leu Arg Ala His Leu Arg Trp
20 25 30

His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly Lys
35 40 45

Arg Phe Thr Arg Ser Asp Glu Leu Gln Arg His Lys Arg Thr His Thr
50 55 60

Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met Arg
65 70 75 80

Ser Asp His Leu Ser Lys His Ile Lys Thr His Gln Asn Lys Lys Gly
85 90 95

Gly Pro Gly Val Ala Leu Ser Val Gly Thr Leu Pro Leu Asp Ser Gly
100 105 110

Ala Gly Ser Glu Gly Ser Gly Thr Ala Thr Pro Ser Ala Leu Ile Thr
115 120 125

Thr Asn Met Val Ala Met Glu Ala Ile Cys Pro Glu Gly Ile Ala Arg
130 135 140

Leu Ala Asn Ser Gly Ile Asn Val Met Gln Val Ala Asp Leu Gln Ser
145 150 155 160

Ile Asn Ile Ser Gly Asn Gly Phe
165

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Gly Ile Val Pro Gln Leu Gln Asn Ile Val Ser Thr Val Asn Leu
1 5 10 15

Gly Cys Lys Leu Asp Leu Lys Thr Ile Ala Leu Arg Ala Arg Asn Ala
20 25 30

Glu Tyr Asn Pro Lys Arg Phe Ala Ala Val Ile Met Arg Ile Arg Glu
35 40 45

Pro Arg Thr Thr Ala Leu Ile Phe Ser Ser Gly Lys Met Val Cys Thr
50 55 60

Gly Ala Lys Ser Glu Glu Gln Ser Arg Leu Ala Ala Arg Lys Tyr Ala
65 70 75 80

Arg Val Val Gln Lys Leu Gly Phe Pro Ala Lys Phe Leu Asp Phe Lys
85 90 95

Ile Gln Asn Met Val Gly Ser Cys Asp Val Lys Phe Pro Ile Arg Leu
100 105 110

Glu Gly Leu Val Leu Thr His Gln Gln Phe Ser Ser Tyr Glu Pro Glu
115 120 125

Leu Phe Pro Gly Leu Ile Tyr Arg Met Ile Lys Pro Arg Ile Val Leu
130 135 140

Leu Ile Phe Val Ser Gly Lys Val Val Leu Thr Gly Ala Lys Val Arg
145 150 155 160

Ala Glu Ile Tyr Glu Ala Phe Glu Asn Ile Tyr Pro Ile Leu Lys Gly
165 170 175

Phe Arg Lys Thr Thr
180

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ser Cys Phe Ala Leu Ile Ser Gly Thr Ala Asn Gln Val Lys Cys Tyr
1 5 10 15

Arg Phe Arg Val Lys Lys Asn His Arg His Arg Tyr Glu Asn Cys Thr
20 25 30

Thr Thr Trp Phe Thr Val Ala Asp Asn Gly Ala Glu Arg Gln Gly Gln
35 40 45

Ala Gln Ile Leu Ile Thr Phe Gly Ser Pro Ser Gln Arg Gln Asp Phe
50 55 60

Leu Lys His Val Pro Leu Pro Pro Gly Met Asn Ile Ser Gly Phe Thr
65 70 75 80

Ala Ser Leu Asp Phe
85

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Cys	Pro	Cys	Leu	Leu	Ile	Gly	Thr	Ser	Gly	Asn	Gly	Asn	Gln	Val	Lys
1					5				10						15

Cys Tyr Ser Phe Arg Val Lys Arg Trp His Asp Arg Asp Lys Tyr His
20 25 30

His	Thr	Thr	Trp	Trp	Ala	Val	Gly	Gly	Gln	Gly	Ser	Glu	Arg	Pro
					35				40				45	

Gly Asp Ala Thr Val Ile Val Thr Phe Lys Asp Gln Ser Gln Arg Ser
50 55 60

His Phe Leu Gln Gln Val Pro Leu Pro Pro Gly Met Ser Ala His Gly
65 70 75 80

Val Thr Met Thr Val Asp Phe
85

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Arg Tyr Arg Leu Lys Ser Lys His Ser Ser Leu Phe Asp Cys Ile Ser
20 25 30

Thr Thr Trp Ser Trp Val Asp Thr Thr Ser Thr Cys Arg Leu Gly Ser
35 40 45

Gly Arg Met Leu Ile Lys Phe Ala Asp Ser Glu Gln Arg Asp Lys Phe
50 55 60

Leu Ser Arg Val Pro Leu Pro Ser Thr Thr Gln Val Phe Leu Gly Asn
65 70 75 80

Phe Tyr Gly Leu

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Pro Pro Val Ile Leu Val Arg Gly Gly Ala Asn Thr Leu Lys Cys Phe
1 5 10 15

Arg Asn Arg Ala Arg Val Arg Tyr Arg Gly Leu Phe Lys Tyr Phe Ser
20 25 30

Thr Thr Trp Ser Trp Val Ala Gly Asp Ser Thr Glu Arg Leu Gly Arg
35 40 45

Ser Arg Met Leu Ile Leu Phe Thr Ser Ala Cys Gln Arg Glu Lys Pro
50 55 60

Asp Glu Thr Val Lys Tyr Pro Lys Gly Val Asp Thr Ser Tyr Gly Asn
65 70 75 80

Leu Asp Ser Leu

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Pro Pro Val Val Cys Val Lys Gly Gly Ala Asn Gln Leu Lys Cys Leu
1 5 10 15

Arg Tyr Arg Leu Lys Ala Ser Thr Gln Val Asp Phe Asp Ser Ile Ser
20 25 30

Thr Thr Trp His Trp Thr Asp Arg Lys Asn Thr Glu Arg Ile Gly Ser
35 40 45

Ala Arg Met Leu Val Lys Phe Ile Asp Glu Ala Gln Arg Glu Lys Phe
50 55 60

Leu Glu Arg Val Ala Leu Pro Arg Ser Val Ser Val Phe Leu Gly Gln
65 70 75 80

Phe Asn Gly Ser

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Thr Pro Ile Val Gln Leu Gln Gly Asp Ser Asn Cys Leu Lys Cys Phe
1 5 10 15

Arg Tyr Arg Leu Asn Asp Lys Tyr Lys His Leu Phe Glu Leu Ala Ser
20 25 30

Ser Thr Trp His Trp Ala Ser Pro Glu Ala Pro His Lys Asn Ala Ile
35 40 45

Val Thr Leu Thr Tyr Ser Ser Glu Glu Gln Arg Gln Gln Phe Leu Asn
50 55 60

Ser Val Lys Ile Pro Pro Thr Ile Arg His Lys Val Gly Phe Met Ser
65 70 75 80

Leu His Leu Leu

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Thr Pro Ile Val Gln Phe Gln Gly Glu Ser Asn Cys Leu Lys Cys Phe
1 5 10 15

Arg Tyr Arg Leu Asn Arg Asp His Arg His Leu Phe Asp Leu Ile Ser
20 25 30

Ser Thr Trp His Trp Ala Ser Ser Lys Ala Pro His Lys His Ala Ile
35 40 45

Val Thr Val Thr Tyr Asp Ser Glu Glu Gln Arg Gln Gln Phe Leu Asp
50 55 60

Val Val Lys Ile Pro Pro Thr Ile Ser His Lys Leu Gly Phe Met Ser
65 70 75 80
Leu His Leu Leu

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr Pro Ile Ile His Leu Lys Gly Asp Arg Asn Ser Leu Lys Cys Leu
1 5 10 15
Arg Tyr Arg Leu Arg Lys His Ser Asp His Tyr Arg Asp Ile Ser Ser
20 25 30
Thr Trp His Trp Thr Gly Ala Gly Asn Glu Lys Thr Gly Ile Leu Thr
35 40 45
Val Thr Tyr His Ser Glu Thr Gln Arg Thr Lys Phe Leu Asn Thr Val
50 55 60
Ala Ile Pro Asp Ser Val Gln Ile Leu Val Gly Tyr Asn Thr Met Tyr
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Thr Pro Ile Val His Leu Lys Gly Asp Ala Asn Thr Leu Lys Cys Leu
1 5 10 15

Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr Thr Ala Val Ser Ser
 20 25 30

Thr Trp His Trp Thr Gly His Asn Tyr Lys His Lys Ser Ala Ile Val
35 40 45

Thr Leu Thr Tyr Asp Ser Glu Trp Gln Arg Asp Gln Phe Leu Ser Gln
 50 55 60

Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly Phe Met Ser Ile
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Ala Pro Ile Val His Leu Lys Gly Glu Ser Asn Ser Leu Lys Cys Leu
 1 5 10 15

Arg Tyr Arg Leu Lys Pro Tyr Asn Glu Leu Tyr Ser Ser Met Ser Ser
 20 25 30

Thr Trp His Trp Thr Ser Asp Asn Lys Asn Ser Lys Asn Gly Ile Val
35 40 45

Thr Val Thr Phe Val Thr Gly Gln Gln Gln Gln Met Phe Leu Gly Thr
50 55 60

Val Lys Ile Pro Pro Thr Val Gln Ile Ser Thr Gly Phe Met Thr Leu
65 70 75 80

Val

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
1 5 10 15

Glu Asn Tyr Cys Asn
20

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
1 5 10 15

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
20 25 30

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Gly Ile Val Glu Gln Cys Cys Ala Ser Val Cys Ser Leu Tyr Gln Leu
1 5 10 15

Glu Asn Tyr Cys Asn
20

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
1 5 10 15

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
20 25 30

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Ile
1 5 10 15

Lys Arg Ser Leu Ala Arg Phe Cys
20

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Asp Ser Trp Met Glu Glu Val Ile Lys Ile Cys Gly Arg Glu Leu Val
1 5 10 15

Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Ser
20 25 30

Leu

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Glu Glu Lys Met Gly Thr Ala Lys Lys Cys Cys Ala Ile Gly Cys Ser
1 5 10 15

Thr Glu Asp Phe Arg Met Val Cys
20

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Arg Pro Asn Trp Glu Glu Arg Ser Arg Leu Cys Gly Arg Asp Leu Ile
1 5 10 15

Arg Ala Phe Ile Tyr Leu Cys Gly Gly Thr Arg Trp Thr Arg Leu Pro
20 25 30

Asn Phe Gly Asn Tyr Pro Ile Met
35 40

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Ser Gly Ile Val Pro Thr Leu Gln Asn Ile Val Ser Thr Val Asn Leu
1 5 10 15

Asp Cys Lys Leu Asp Leu Lys Ala Ile Ala Leu Gln Ala Arg Asn Ala
20 25 30

Glu Tyr Asn Pro Lys Arg Phe Ala Ala Val Ile Met Arg Ile Arg Glu
35 40 45

Pro Lys Thr Thr Ala Leu Ile Phe Ala Ser Gly Lys Met Val Cys Thr
50 55 60

Gly Ala Lys Ser Glu Asp Phe Ser Lys Met Ala Ala Arg Lys Tyr Ala
65 70 75 80

Arg Ile Val Gln Lys Leu Gly Phe Pro Ala Lys Phe Lys Asp Phe Lys
85 90 95

Ile Gln Asn Ile Val Gly Ser Cys Asp Val Lys Phe Pro Ile Arg Leu
100 105 110

Glu Gly Leu Ala Tyr Ser His Ala Ala Phe Ser Ser Tyr Glu Pro Glu
115 120 125

Leu Phe Pro Gly Leu Ile Tyr Arg Met Lys Val Pro Lys Ile Val Leu
130 135 140

Leu Ile Phe Val Ser Gly Lys Ile Val Ile Thr Gly Ala Lys Met Arg
145 150 155 160

Asp Glu Thr Tyr Lys Ala Phe Glu Asn Ile Tyr Pro Val Leu Ser Glu
165 170 175

Phe Arg Lys Ile Gln Gln
180

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asn Ser Asn Ser Thr Pro Ile Val His Leu Lys Gly Asp Ala Asn Thr
1 5 10 15

Leu Lys Cys Leu Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr Thr
20 25 30

Ala Val Ser Ser Thr Trp His Trp Thr Gly His Asn Val Lys His Lys
35 40 45

Ser Ala Ile Val Thr Leu Thr Tyr Asp Ser Glu Trp Gln Arg Asp Gln
50 55 60

Phe Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly
65 70 75 80

Phe Met Ser Ile

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Asn Ser Asn Thr Thr Pro Ile Val His Leu Lys Gly Asp Ala Asn Thr
1 5 10 15

Leu Lys Cys Leu Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr Thr
20 25 30

Ala Val Ser Ser Thr Trp His Trp Thr Gly His Asn Val Lys His Lys
35 40 45

Ser Ala Ile Val Thr Leu Thr Tyr Asp Ser Glu Trp Gln Arg Asp Gln
50 55 60

Phe Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly
65 70 75 80

Phe Met Ser Ile

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Ser Gly Asn Thr Thr Pro Ile Ile His Leu Lys Gly Asp Arg Asn Ser
1 5 10 15

Leu Lys Cys Leu Arg Tyr Arg Leu Arg Lys His Ser Asp His Tyr Arg
20 25 30

Asp Ile Ser Ser Thr Trp His Trp Thr Gly Ala Gly Asn Glu Lys Thr
35 40 45

Gly Ile Leu Thr Val Thr Tyr His Ser Glu Thr Gln Arg Thr Lys Phe
50 55 60

Leu Asn Thr Val Ala Ile Pro Asp Ser Val Gln Ile Leu Val Gly Tyr
65 70 75 80

Met Thr Met

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser Gly Asn Thr Ala Pro Ile Val His Leu Lys Gly Glu Ser Asn Ser
1 5 10 15

Leu Lys Cys Leu Arg Tyr Arg Leu Lys Pro Tyr Lys Glu Leu Tyr Ser
20 25 30

Ser Met Ser Ser Thr Trp His Trp Thr Ser Asp Asn Lys Asn Ser Lys
35 40 45

Asn Gly Ile Val Thr Val Thr Phe Val Thr Glu Gln Gln Gln Met
50 55 60

Phe Leu Gly Thr Val Lys Ile Pro Pro Thr Val Gln Ile Ser Thr Gly
65 70 75 80

Phe Met Thr Leu

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ser Gly Asn Thr Ser Cys Phe Ala Leu Ile Ser Gly Thr Ala Asn Gln
1 5 10 15

Val Lys Cys Tyr Arg Phe Arg Val Lys Lys Asn His Arg His Arg Tyr
20 25 30

Glu Asn Cys Thr Thr Trp Phe Thr Val Ala Asp Asn Gly Ala Glu
35 40 45

Arg Gln Gly Gln Ala Gln Ile Leu Ile Thr Phe Gly Ser Pro Ser Gln
50 55 60

Arg Gln Asp Phe Leu Lys His Val Pro Leu Pro Pro Gly Met Asn Ile
65 70 75 80

Ser Gly Phe Thr Ala Ser Leu Asp Phe
85

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Ser Asn Lys Lys Thr Thr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Asn Ser Asn Thr
1

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ser Gly Asn Thr
1

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Ser Ser Gly Ser Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Cys Tyr Pro Glu Ile Lys Asp Lys Glu Glu Val Gln Arg Lys Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Glu Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
50 55 60

Thr Ala
65

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Met Glu Gln Glu Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
50 55 60

Thr Ala
65

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
50 55 60

Thr Ala
65

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Ser Thr Lys Lys Lys Pro Leu Thr Gln Glu Gln Leu Glu Asp Ala Arg
1 5 10 15

Arg Leu Lys Ala Ile Tyr Glu Lys Lys Asn Glu Leu Gly Leu Ser
20 25 30

Gln Glu Ser Val Ala Asp Lys Met Gly Met Gly Gln Ser Gly Val Gly
35 40 45

Ala Leu Phe Asn Gly Ile Asn Ala Leu Asn Ala Tyr Asn Ala Ala Leu
50 55 60

Leu Ala Lys Ile Leu Lys Val Ser Val Glu Glu Phe Ser Pro Ser Ile
65 70 75 80

Ala Arg Glu Ile Tyr Glu Met Tyr Glu Ala Val Ser Met Glu Pro Ser
85 90 95

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Ser Thr Lys Lys Pro Leu Thr Gln Glu Gln Leu Glu Asp Ala Arg
1 5 10 15

Arg Leu Lys Ala Ile Tyr Glu Lys Lys Asn Glu Leu Gly Leu Ser
20 25 30

Gln Glu Ser Val Ala Asp Lys Met Gly Met Gly Gln Ser Gly Val Gly
35 40 45

Ala Leu Phe Asn Gly Ile Asn Ala Leu Asn Ala Tyr Asn Ala Ala Leu
50 55 60

Leu Ala Lys Ile Leu Lys Val Ser Val Glu Glu Phe Ser Pro Ser Ile
65 70 75 80

Ala Arg Glu Ile Tyr Glu Met Cys Glu Ala Val Ser Met Glu Pro Ser
85 90 95

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
1 5 10 15

Glu Asn Tyr Cys Asn Met Ser Met Glu Gln Arg Ile Thr Leu Lys Asp
20 25 30

Tyr Ala Met Arg Phe Gly Gln Thr Lys Thr Ala Lys Asp Leu Gly Val
35 40 45

Tyr Gln Ser Ala Ile Asn Lys Ala Ile His Ala Gly Arg Lys Ile Phe
50 55 60

Leu Thr Ile Asn Ala Asp Gly Ser Val Tyr Ala Glu Glu Val Lys Pro
65 70 80

Phe Pro Ser Asn Lys Lys Thr Thr Ala Ser Asn Lys Lys Thr Thr Ala
85 90 95

Asn Ser Asn Thr Thr Pro Ile Val His Leu Lys Gly Asp Ala Asn Thr
100 105 110

Leu Lys Cys Leu Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr Thr
115 120 125

Ala Val Ser Ser Thr Trp His Trp Thr Gly His Asn Val Lys His Lys
130 135 140

Ser Ala Ile Val Thr Leu Thr Tyr Asp Ser Glu Trp Gln Arg Asp Gln
145 150 160

Phe Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly
 165 170 175

Phe Met Ser Ile
180

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
1 5 10 15

Glu Asn Tyr Cys Asn Met Ser Met Glu Gln Arg Ile Thr Leu Lys Asp
20 25 30

Tyr Ala Met Arg Phe Gly Gln Thr Lys Thr Ala Lys Asp Leu Gly Val
35 40 45

Tyr Gln Ser Ala Ile Asn Lys Ala Ile His Ala Gly Arg Lys Ile Phe
50 55 60

Leu Thr Ile Asn Ala Asp Gly Ser Val Tyr Ala Glu Glu Val Lys Pro
65 70 75 80

Phe Pro Ser Asn Lys Lys Thr Thr Ala Ser Asn Lys Lys Thr Thr Ala

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
1 5 10 15

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Met Ser
20 25 30

Met Glu Gln Glu Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
35 40 45

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
50 55 60

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
65 70 75 80

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
85 90 95

Thr Ala Ser Asn Lys Lys Thr Thr Ala Ser Ser Gly Ser Ser Gly Ser
100 105 110

Gly Ile Val Pro Gln Leu Gln Asn Ile Val Ser Thr Val Asn Leu Gly
115 120 125

Cys Lys Leu Asp Leu Lys Thr Ile Ala Leu Arg Ala Arg Asn Ala Glu
130 135 140

Tyr Asn Pro Lys Arg Phe Ala Ala Val Ile Met Arg Ile Arg Glu Pro
145 150 155 160

Arg Thr Thr Ala Leu Ile Phe Ser Ser Gly Lys Met Val Cys Thr Gly
165 170 175

Ala Lys Ser Glu Glu Gln Ser Arg Leu Ala Ala Arg Lys Tyr Ala Arg
180 185 190

Val Val Gln Lys Leu Gly Phe Pro Ala Lys Phe Leu Asp Phe Lys Ile
 195 200 205

 Gln Asn Met Val Gly Ser Cys Asp Val Lys Phe Pro Ile Arg Leu Glu
 210 215 220

 Gly Leu Val Leu Thr His Gln Gln Phe Ser Ser Tyr Glu Pro Glu Leu
 225 230 235 240

 Phe Pro Gly Leu Ile Tyr Arg Met Ile Lys Pro Arg Ile Val Leu Leu
 245 250 255

 Ile Phe Val Ser Gly Lys Val Val Leu Thr Gly Ala Lys Val Arg Ala
 260 265 270

 Glu Ile Tyr Glu Ala Phe Glu Asn Ile Tyr Pro Ile Leu Lys Gly Phe
 275 280 285

 Arg Lys Thr Thr
 290

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
 1 5 10 15

 Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Met Ser
 20 25 30

 Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
 35 40 45

 Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
 50 55 60

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
 65 70 75 80

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
 85 90 95

Thr Ala Ser Asn Lys Lys Thr Thr Ala Gly Asp Pro Gly Lys Lys Lys
 100 105 110

Gln His Ile Cys His Ile Gln Gly Cys Gly Lys Val Tyr Gly Lys Thr
 115 120 125

Ser His Leu Arg Ala His Leu Arg Trp His Thr Gly Glu Arg Pro Phe
 130 135 140

Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg Phe Thr Arg Ser Asp Glu
 145 150 155 160

Leu Gln Arg His Lys Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys
 165 170 175

Pro Glu Cys Pro Lys Arg Phe Met Arg Ser Asp His Leu Ser Lys His
 180 185 190

Ile Lys Thr His Gln Asn Lys Lys Gly Gly Pro Gly Val Ala Leu Ser
 195 200 205

Val Gly Thr Leu Pro Leu Asp Ser Gly Ala Gly Ser Glu Gly Ser Gly
 210 215 220

Thr Ala Thr Pro Ser Ala Leu Ile Thr Thr Asn Met Val Ala Met Glu
 225 230 235 240

Ala Ile Cys Pro Glu Gly Ile Ala Arg Leu Ala Asn Ser Gly Ile Asn
 245 250 255

Val Met Gln Val Ala Asp Leu Gln Ser Ile Asn Ile Ser Gly Asn Gly
 260 265 270

Phe

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Ile
1 5 10 15

Lys Arg Ser Leu Ala Arg Phe Cys Met Ser Met Arg Gln Arg Ile Thr
20 25 30

Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln Thr Lys Thr Ala Lys Asp
35 40 45

Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys Ala Ile His Ala Gly Arg
50 55 60

Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly Ser Val Tyr Ala Glu Glu
65 70 75 80

Val Lys Pro Phe Pro Ser Asn Lys Lys Thr Thr Ala Ser Asn Lys Lys
85 90 95

Thr Thr Ala Met Ala Asp Asp Asp Pro Tyr Gly Thr Gly Gln Met Phe
100 105 110

His Leu Asn Thr Ala Leu Thr His Ser Ile Phe Asn Ala Glu Leu Tyr
115 120 125

Ser Pro Glu Ile Pro Leu Ser Thr Asp Gly Pro Tyr Leu Gln Ile Leu
130 135 140

Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly
145 150 155 160

Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys
165 170 175

Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val
180 185 190

Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His
195 200 205

Ser Leu Val Gly Lys His Cys Glu Asp Gly Val Cys Thr Val Thr Ala
210 215 220

Gly Pro Lys Asp Met Val Val Gly Phe Ala Asn Leu Gly Ile Leu His
 225 230 235 240

 Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu
 245 250 255

 Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Ser Asp Leu
 260 265 270

 Ala Tyr Leu Gln Ala Glu Gly Gly Asp Arg Gln Leu Thr Asp Arg
 275 280 285

 Glu Lys Glu Ile Ile Arg Gln Ala Ala Val Gln Gln Thr Lys Glu Met
 290 295 300

 Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser
 305 310 315 320

 Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile
 325 330 335

 Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met
 340 345 350

 Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu
 355 360 365

 Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu
 370 375 380

 Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr
 385 390 395 400

 Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys
 405 410 415

 Asp Val Asn Ile Thr
 420

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
 50 55 60

Thr Ala Met Ala Glu Asp Asp Pro Tyr Leu Gly Arg Pro Glu Gln Met
65 70 75 80

Phe His Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val
85 90 95

Phe Gln Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln
 100 105 110

Ile Leu Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys
115 120 125

Glu Gly Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn
130 135 140

Lys Lys Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala
 145 150 155 160

Lys Val Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His
165 170 175

Ala His Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val
 180 185 190

Thr Ala Gly Pro Glu Asp Cys Val His Gly Phe Ala Asn Leu Gly Ile
195 200 205

Leu His Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met
210 215 220

Thr Glu Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro
225 230 235 240

Asp Leu Ala Tyr Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Gly
245 250 255

Asp Arg Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys
260 265 270

Glu Met Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro
275 280 285

Asp Ser Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp
290 295 300

Ala Ile Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val
305 310 315 320

Arg Met Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr
325 330 335

Leu Leu Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr
340 345 350

Glu Glu Glu Asn Gly Val Trp Glu Gly Phe Gly Asp Phe Ser
355 360 365

Pro Thr Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys
370 375 380

Tyr Lys Asp Ile Asn Ile Thr
385 390

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Glu Gln Glu Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
 20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
 35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
 50 55 60

Thr Ala Met Ala Glu Asp Asp Pro Tyr Leu Gly Arg Pro Glu Gln Met
 65 70 75 80

Phe His Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val
 85 90 95

Phe Gln Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln
 100 105 110

Ile Leu Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys
 115 120 125

Glu Gly Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn
 130 135 140

Lys Lys Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala
 145 150 155 160

Lys Val Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His
 165 170 175

Ala His Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val
 180 185 190

Thr Ala Gly Pro Glu Asp Cys Val His Gly Phe Ala Asn Leu Gly Ile
 195 200 205

Leu His Val Thr Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met
 210 215 220

Thr Glu Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro
 225 230 235 240

Asp Leu Ala Tyr Leu Gln Ala Glu Gly Gly Asp Arg Gln Leu Gly
 245 250 255

Asp Arg Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys
 260 265 270

Glu Met Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro
 275 280 285

A1

Asp Ser Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp
 290 295 300

Ala Ile Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val
 305 310 315 320

Arg Met Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr
 325 330 335

Leu Leu Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr
 340 345 350

Glu Glu Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser
 355 360 365

Pro Thr Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys
 370 375 380

Tyr Lys Asp Ile Asn Ile Thr
 385 390

G1 (2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
 1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
 20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
 35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
 50 55 60

Thr Ala Ser Asn Lys Lys Thr Thr Ala Gly Asp Pro Gly Lys Lys Lys
 65 70 75 80

Gln His Ile Cys His Ile Gln Gly Cys Gly Lys Val Tyr Gly Lys Thr
 85 90 95

Ser His Leu Arg Ala His Leu Arg Trp His Thr Gly Glu Arg Pro Phe
 100 105 110

Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg Phe Thr Arg Ser Asp Glu
 115 120 125

Leu Gln Arg His Lys Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys
 130 135 140

Pro Glu Cys Pro Lys Arg Phe Met Arg Ser Asp His Leu Ser Lys His
 145 150 155 160

Ile Lys Thr His Gln Asn Lys Lys Gly Gly Pro Gly Val Ala Leu Ser
 165 170 175

Val Gly Thr Leu Pro Leu Asp Ser Gly Ala Gly Ser Glu Gly Ser Gly
 180 185 190

Thr Ala Thr Pro Ser Ala Leu Ile Thr Thr Asn Met Val Ala Met Glu
 195 200 205

Ala Ile Cys Pro Glu Gly Ile Ala Arg Leu Ala Asn Ser Gly Ile Asn
 210 215 220

Val Met Gln Val Ala Asp Leu Gln Ser Ile Asn Ile Ser Gly Asn Gly
 225 230 235 240

Phe

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGGAMTNYCC

10

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30

His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Ala His Gln Asn Ser Gln Thr
50 55 60

His Gln Ala Ser Leu Ser Lys Gln
65 70